

Figure 1. Sequence of *C. pneumoniae* ATP-binding cassette gene

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acttcccccc tgctaaacta tgctcagata atgctgctat gattgcaggt ctagggggag 60
aaaattttca aaaaaactct agtattccgg aaattcgtat atg cgc aag ata tca    115
                                     Met Arg Lys Ile Ser
                                     1          5

gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa    163
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln
                                     10          15          20

ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct    211
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala
                                     25          30          35

att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga    259
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg
                                     40          45          50

ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt    307
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val
                                     55          60          65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac    355
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp
                                     70          75          80          85

tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca    403
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser
                                     90          95          100

gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa    451
Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu
                                     105          110          115

tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt    499
Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe
                                     120          125          130

gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc    547
Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu
                                     135          140          145

tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt    595
Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val
                                     150          155          160          165

gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt    643
Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu
                                     170          175          180

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"66010" 2931/0246

cca	gtc	ttt	ttc	ccc	gtt	cat	aaa	tct	caa	aga	acc	ctg	caa	tcc	aaa	691
Pro	Val	Phe	Phe	Pro	Val	His	Lys	Ser	Gln	Arg	Thr	Leu	Gln	Ser	Lys	
			185					190						195		
tct	cta	cct	ata	gca	agc	gga	gct	ttc	tat	cct	aaa	aat	atc	aaa	caa	739
Ser	Leu	Pro	Ile	Ala	Ser	Gly	Ala	Phe	Tyr	Pro	Lys	Asn	Ile	Lys	Gln	
		200					205					210				
aaa	caa	tgg	ata	aaa	ctc	tca	aaa	aac	cct	cac	tac	tat	aat	caa	agt	787
Lys	Gln	Trp	Ile	Lys	Leu	Ser	Lys	Asn	Pro	His	Tyr	Tyr	Asn	Gln	Ser	
	215					220					225					
cag	gtg	gaa	act	aaa	acg	att	acg	att	cac	ttc	att	ccc	gat	gca	aac	835
Gln	Val	Glu	Thr	Lys	Thr	Ile	Thr	Ile	His	Phe	Ile	Pro	Asp	Ala	Asn	
230					235					240					245	
aca	gca	gca	aaa	cta	ttt	aat	cag	gga	aaa	ctc	aat	tgg	caa	gga	cct	883
Thr	Ala	Ala	Lys	Leu	Phe	Asn	Gln	Gly	Lys	Leu	Asn	Trp	Gln	Gly	Pro	
			250						255					260		
cct	tgg	gga	gaa	cgc	att	cct	caa	gaa	acc	cta	tcc	aat	tta	cag	tct	931
Pro	Trp	Gly	Glu	Arg	Ile	Pro	Gln	Glu	Thr	Leu	Ser	Asn	Leu	Gln	Ser	
			265					270					275			
aag	ggg	cac	tta	cac	tct	ttt	gat	gtc	gca	gga	acc	tca	tgg	ctc	acc	979
Lys	Gly	His	Leu	His	Ser	Phe	Asp	Val	Ala	Gly	Thr	Ser	Trp	Leu	Thr	
		280					285					290				
ctc	aat	atc	aat	aaa	ttc	ccc	ctc	aac	aat	atg	aag	ctt	aga	gaa	gcc	1027
Phe	Asn	Ile	Asn	Lys	Phe	Pro	Leu	Asn	Asn	Met	Lys	Leu	Arg	Glu	Ala	
	295					300					305					
tta	gca	tca	gcc	tta	gat	aag	gaa	gct	ctt	gtc	tca	act	ata	ttc	tta	1075
Leu	Ala	Ser	Ala	Leu	Asp	Lys	Glu	Ala	Leu	Val	Ser	Thr	Ile	Phe	Leu	
310					315					320					325	
ggc	cgt	gca	aaa	act	gcc	gat	cat	ctc	cta	cct	aca	aat	att	cat	agc	1123
Gly	Arg	Ala	Lys	Thr	Ala	Asp	His	Leu	Leu	Pro	Thr	Asn	Ile	His	Ser	
				330					335					340		
at	ccc	gaa	cat	caa	aaa	caa	gag	atg	gca	caa	cgc	caa	gct	tac	gct	1171
Tyr	Pro	Glu	His	Gln	Lys	Gln	Glu	Met	Ala	Gln	Arg	Gln	Ala	Tyr	Ala	
			345					350					355			
aa	aaa	ctc	ttt	aaa	gaa	gct	tta	gaa	gaa	ctc	caa	atc	act	gct	aaa	1219
Lys	Lys	Leu	Phe	Lys	Glu	Ala	Leu	Glu	Glu	Leu	Gln	Ile	Thr	Ala	Lys	
		360					365					370				
at	ctc	gaa	cat	ctt	aat	ctt	atc	ttt	ccc	gtt	tcc	tcg	tca	gca	agt	1267
asp	Leu	Glu	His	Leu	Asn	Leu	Ile	Phe	Pro	Val	Ser	Ser	Ser	Ala	Ser	
	375					380					385					

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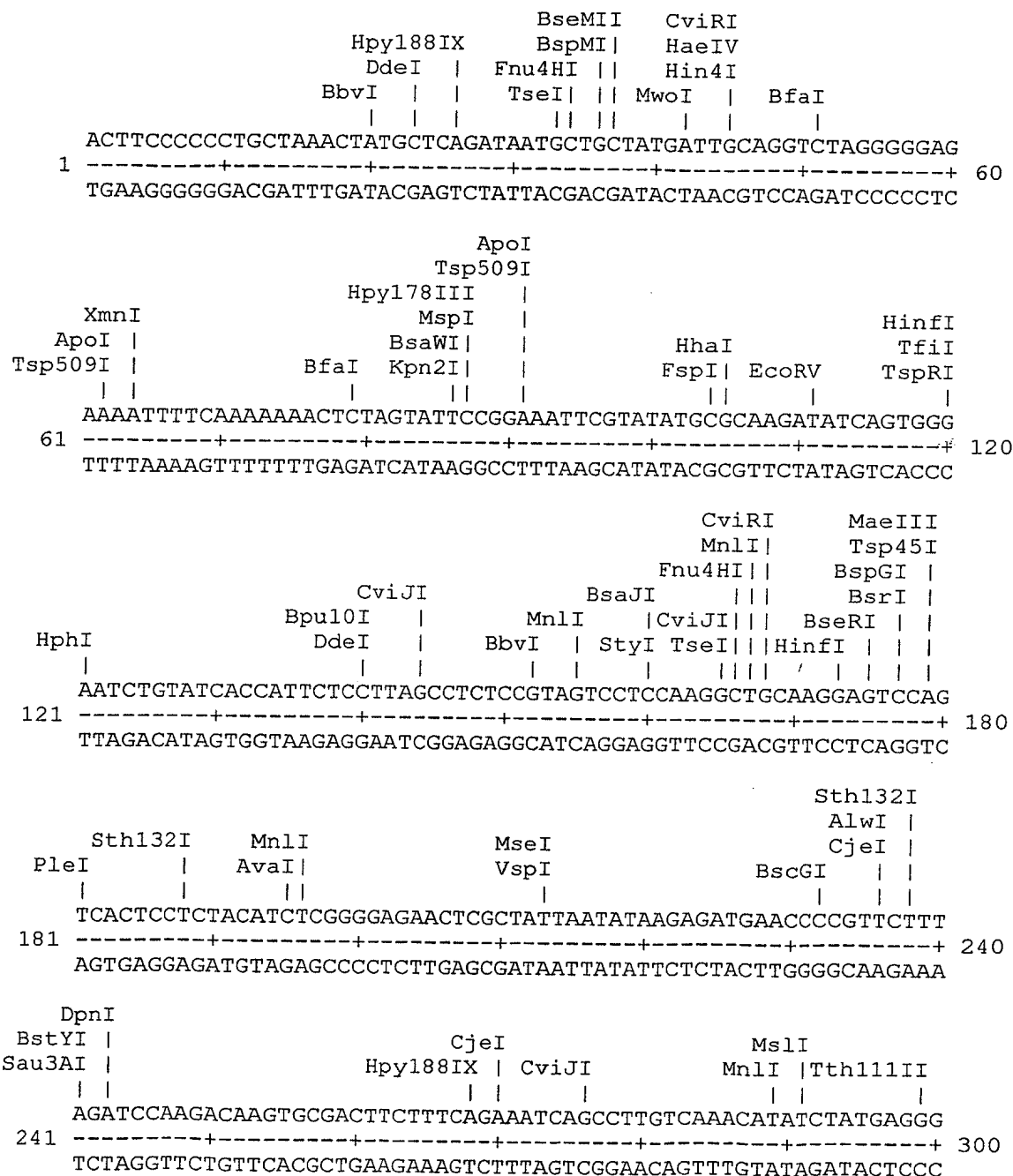
Figure 1 Cont.

tct tta cta gtc caa ctt ata cga gaa cag tgg aaa gaa agt tta ggg	1315
Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp Lys Glu Ser Leu Gly	
390 395 400 405	
ttc gct atc cct att gtc gga aag gaa ttt gct ctt ctc caa gca gac	1363
Phe Ala Ile Pro Ile Val Gly Lys Glu Phe Ala Leu Leu Gln Ala Asp	
410 415 420	
cta tct tca ggg aac ttc tct tta gct aca gga gga tgg ttc gca gac	1411
Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly Gly Trp Phe Ala Asp	
425 430 435	
ttt gct gat cct atg gca ttt cta acg atc ttt gct tat cca tca gga	1459
Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe Ala Tyr Pro Ser Gly	
440 445 450	
gtt cct cct tat gca atc aac cat aag gac ttc cta gaa att cta caa	1507
Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe Leu Glu Ile Leu Gln	
455 460 465	
aac ata gaa caa gag caa gat cac caa aaa cgc tcg gaa tta gtg tcg	1555
Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg Ser Glu Leu Val Ser	
470 475 480 485	
caa gct tct ctt tac cta gag acc ttt cat att att gag cgc atc tac	1603
Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile Ile Glu Pro Ile Tyr	
490 495 500	
cac gac gca ttt caa ttt gct atg aat aaa aaa ctt tct aat cta gga	1651
His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys Leu Ser Asn Leu Gly	
505 510 515	
gtc tca cca aca gga gtt gtg gac ttc cgt tat gct aag gaa aat	1696
Val Ser Pro Thr Gly Val Val Asp Phe Arg Tyr Ala Lys Glu Asn	
520 525 530	
tagcacctct tttaatctcg caaacttgctc aagaactgaa tcttatacta aactgggtgc	1756
ctttgtggca cctcggtttcc ttctgactgc tcttctctct cta	1799

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Figure 2. Restriction enzyme analysis of the *C. pneumoniae* ATP-binding cassette gene



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Figure 2 Cont.

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                                Cac8I
Hpy178III   Hpy178III   CviJI |   CviRI   BbsI
|           |           |   |           |
ATTAGTTCAAGAAAATAATCTTTTCAGGAAATATAGAGCCTGCTCTTGCAGAAGACTACTC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TAATCAAGTTCTTTTATTAGAAAGTCCTTTATATCTCGGACGAGAACGTCTTCTGATGAG

                                Hpy188IX
                                PleI|
                                BsaJI | | MnlI
MboII | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
TCTTTCCTCGGACGGACTCACTTATACTTTTAAACTGAAATCAGCTTTTGGAGTAATGG
361 -----+-----+-----+-----+-----+-----+-----+ 420
AGAAAGGAGCCTGCCTGAGTGAATATGAAATTTGACTTTAGTCGAAAACCTCATTACC

                                AluI
                                CviJI   HinfI   Hpy178III
                                MspAII   MboII Bce83I   SmlI |
SimI   MseI PvuII   BbsI TfiI Eco57I   AluI | |
| | | | | | | | | | | | | | | | | | | | | |
CGACCCCTTAACAGCTGAAGACTTTATAGAATCTTGAAACAAGTAGCTACTCAAGAAGT
421 -----+-----+-----+-----+-----+-----+-----+ 480
GCTGGGGAATTGTCGACTTCTGAAATATCTTAGAACCTTTGTTCATCGATGAGTTCTTCA

                                DpnI
                                HinfI   MnlI |
                                TfiI   BstYI | |
                                BsmAI |   Sau3AI | |
Hpy178III | |   Tsp509I | |   AlwI | | |
DdeI | | |   BseMII   TfiI | |   RsaI | | |
| | | | | | | | | | | | | | | | | | | | | |
CTCAGGAATCTATGCTTTTGCCTTGAATCCAATTAAAAATGTACGAAAGATCCAAGAGGG
481 -----+-----+-----+-----+-----+-----+-----+ 540
GAGTCCTTAGATACGAAAACGGAACCTTAGGTTAATTTTACATGCTTTCTAGGTTCTCCC

                                BseSI
                                BsiHKAI
                                Bsp1286I
                                CviRI |
                                MnlI   MjaIV |   HinfI   BsaJI
BsmFI |   ApaLI | |   TfiI   EcoRII
| | | | | | | | | | | | | | | | | | | | | |
ACACCTCTCCATAGACCATTTTGGAGTGCACCTCTCCTAATGAATCTACACTTGTGTGTTAC
541 -----+-----+-----+-----+-----+-----+-----+ 600
TGTGGAGAGGTATCTGGTAAAACCTCACGTGAGAGGATTACTTAGATGTGAACAACAATG

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Figure 2 Cont.

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                                AluI
                                CviJI
                                EarI
HinfI      TfiI      MseI      CjePI |      SapI
ScrFI |      MnlI | MboII |      BsrI |      BscGI
| |      | |      | |      | |      | |
CCTGGAATCCCCAACCTCGCATTTCTTAAACTTTTAGCTCTTCCAGTCTTTTCCCCGT
601 -----+-----+-----+-----+-----+-----+-----+ 660
GGACCTTAGGGGTGGAGCGTAAAGAATTTGAAAATCGAGAAGGTCAGAAAAAGGGCA

                                AluI
                                CviJI
                                MwoI |
                                AciI | |
Sth132I CjePI      CviRI      SfcI      Cac8I | | |
| |      | |      | |      | |      | | |
TCATAAATCTCAAAGAACCCTGCAATCCAAATCTCTACCTATAGCAAGCGGAGCTTTCTA
661 -----+-----+-----+-----+-----+-----+-----+ 720
AGTATTTAGAGTTTCTTGGGACGTTAGGTTTAGAGATGGATATCGTTCGCCTCGAAAGAT

                                Tth111II
                                MnlI
TCCTAAAAATATCAAACAAAAACAATGGATAAACTCTCAAAAAACCCTCACTACTATAA
721 -----+-----+-----+-----+-----+-----+-----+ 780
AGGATTTTTATAGTTTGTTTTGTACCTATTTTGAGAGTTTTTTGGGAGTGATGATATT

                                Sth132I      Fnu4HI
                                HinfI      Hpy178III |      TseI |
                                TfiI      SfaNI |      CviRI | MwoI | |
                                | |      | |      | |      | |
TCAAAGTCAGGTGGAAACTAAAACGATTACGATTCACTTCATTCCCGATGCAAACACAGC
781 -----+-----+-----+-----+-----+-----+-----+ 840
AGTTTCAGTCCACCTTTGATTTTGCTAATGCTAAGTGAAGTAAGGGCTACGTTTGTGTCG

                                AvaII      MnlI
                                EcoO109I      Bce83I |
                                Psp5II      BslI | |
                                MseI      BbvI |      MunI      Sau96I      BsaJI | |      BsmI
                                | |      | |      | |      | |      | |
Tth111II      Tsp509I      Sse8647I      StyI | | |      XmnI
| |      | |      | |      | |      | |      | |
AGCAAACTATTTAATCAGGGAAACTCAATTGGCAAGGACCTCCTTGGGGAGAACGCAT
841 -----+-----+-----+-----+-----+-----+-----+ 900
TCGTTTTGATAAATTAGTCCCTTTGAGTTAACCGTTCCTGGAGGAACCCCTCTTGCGTA

                                BseSI
Hpy178III      Tsp509I      DdeI      Bsp1286I
SmlI |      MnlI |      Bst4CI |      BmgI |
| |      | |      | |      | |
TCCTCAAGAAACCCTATCCAATTTACAGTCTAAGGGCACTTACACTCTTTTGATGTCGC
901 -----+-----+-----+-----+-----+-----+-----+ 960
AGGAGTTCTTTGGGATAGGTTAAATGTCAGATTCCCCGTGAATGTGAGAAAACCTACAGCG

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Figure 2 Cont.

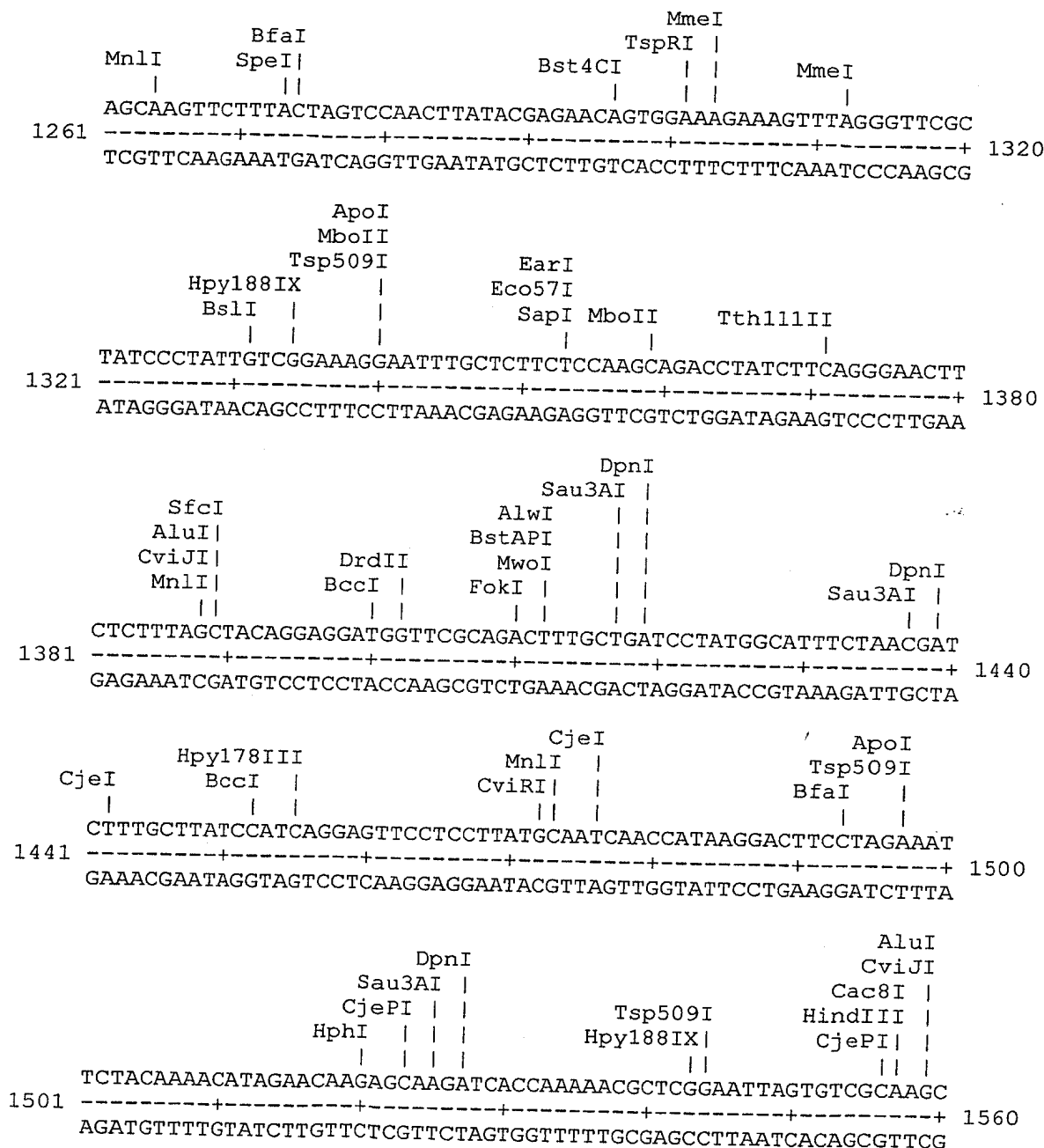
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Figure 2 Cont.

MnlI  
 CviJI  
 NlaIII  
 HphI  
 NlaIV  
 ApoI  
 Tsp509I  
 DdeI  
 AluI  
 CviJI  
 HindIII  
 MnlI  
 961  
 AGGAACCTCATGGCTCACCTTCAATATCAATAAATCCCCCTCAACAATATGAAGCTTAG  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
 TCCTTGGAGTACCGAGTGAAGTTATAGTTATTTAAGGGGGAGTTGTTATACTTCGAATC  
 Bpu10I SfaNI  
 DdeI DdeI  
 CviJI CviJI  
 AluI BceI  
 CviJI BsmAI  
 CviJI HaeIII  
 1021  
 AGAAGCCTTAGCATCAGCCTTAGATAAGGAAGCTCTTGTCTCAACTATATTCTTAGGCCG  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
 TCTTCGGAATCGTAGTCGGAATCTATTCTTCGAGAACAGAGTTGATATAAGAATCCGGC  
 DpnI  
 Sau3AI  
 BstAPI  
 CviRI MwoI  
 Hpy178III  
 AluI Sth132I  
 SspI CviJI CjeI  
 1081  
 TGCAAAAACCTGCCGATCATCTCTACCTACAAATATTCATAGCTATCCCGAACATCAAAA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
 ACGTTTTTGTACGGCTAGTAGAGGATGGATGTTTATAAGTATCGATAGGGCTTGTAGTTTT  
 AluI  
 CviJI  
 HindIII  
 DraI  
 MseI  
 BccI HindIII  
 1141  
 ACAAGAGATGGCACAACGCCAAGCTTACGCTAAAAAACTCTTTAAAGAAGCTTTAGAAGA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
 TGTCTCTACCGTGTTCGGGTCGAATGCGATTTTTTGTAGAAATTTCTTCGAAATCTTCT  
 TaqI  
 Hpy178III  
 DpnI  
 BglIII  
 BstYI  
 Sau3AI  
 TspRI  
 BtsI  
 MboII  
 MseI  
 Sth132I  
 BscGI  
 1201  
 ACTCCAAATCACTGCTAAAGATCTCGAACATCTTAATCTTATCTTTCCCGTTTCCTCGTC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
 TGAGGTTTAGTGACGATTTCTAGAGCTTGTTAGAATTAGAATAGAAAGGGCAAAGGAGCAG

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Figure 2 Cont.





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Figure 2 Cont.

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      BfaI      DpnI
      BsaI |      Sau3AI |
      BsmAI |      CviJI | |
      | |      | | |
1561 TTCTCTTTACCTAGAGACCTTTTCATATTATTGAGCCGATCTACCACGACGCATTTCAATT
-----+-----+-----+-----+-----+-----+-----+-----+ 1620
      AAGAGAAATGGATCTCTGGAAAGTATAATAACTCGGCTAGATGGTGCTGCGTAAAGTTAA

                        HinfI
                        CjeI |
                        HphI | |      PleI
                        BfaI | |      BsmAI |      MjaIV
                        | | |      | |
1621 TGCTATGAATAAAAAAAGTTTCTAATCTAGGAGTCTCACCAACAGGAGTTGTGGACTTCCG
-----+-----+-----+-----+-----+-----+-----+ 1680
      ACGATACTTATTTTTTGAAGATTAGATCCTCAGAGTGGTTGTCTCAACACCTGAAGGC

      Bpu10I
      DdeI
      CjeI | Tsp509I
      | | |
1681 TTATGCTAAGGAAAATTAGCACCTCTTTTAATCTCGCAAAGTTGTCAAGAAGTGAATCTT
-----+-----+-----+-----+-----+-----+-----+ 1740
      AATACGATTCCTTTTAATCGTGGAGAAAATTAGAGCGTTTGAACAGTTCTTGACTTAGAA

      NlaIV      NlaIV
      BsrI |      BanI |
      BanI | |      BglI | |
      BmrI | | |      MwoI | |
      | | |      | | |
1741 ATACTAAAGTGGGTGCCTTTGTGGCACCTCGTTTCCTTCTGACTGCTCTTCTCTCTA
-----+-----+-----+-----+-----+-----+-----+ 1799
      TATGATTTGACCCACGGAAACACCGTGGAGCAAAGGAAGACTGACGAGAAGAGAGAT

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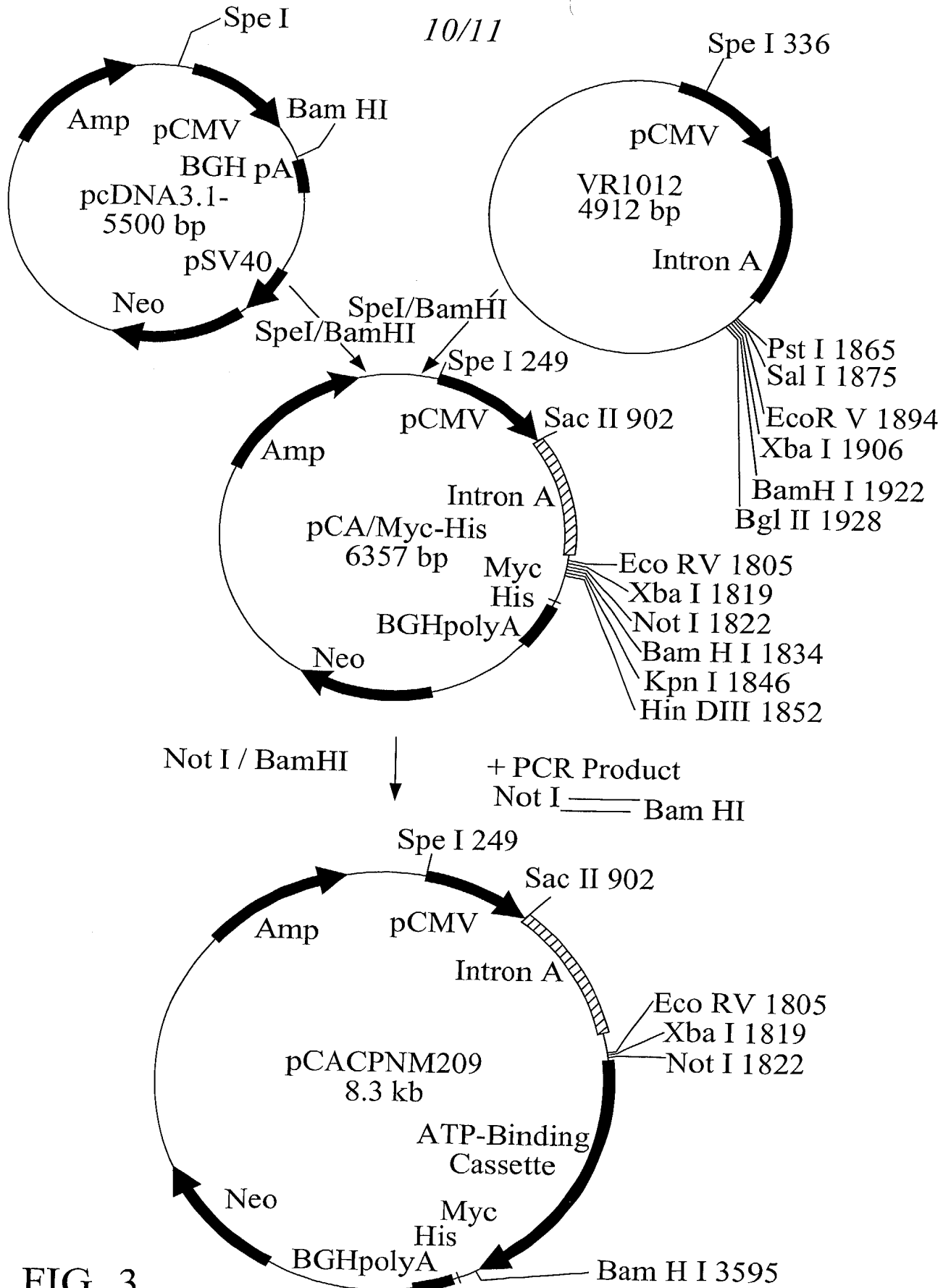


FIG. 3  
Construction of pCACPNM209

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Figure 4: Protective efficacy of DNA immunization with pCACPMM209

